

$$= \frac{1}{\pi} \int_0^\pi \left[\cos^2(\theta) + \sin^2(\theta) \right] d\theta = \frac{1}{\pi} \int_0^\pi 1 d\theta = \frac{1}{\pi} [\theta]_0^\pi = \frac{1}{\pi} (\pi - 0) = 1$$

Kohr, W.: Fyelding, C.: Lam, R.

RESULT 7

C64884

Y340 protein - Escherichia coli

N: Alternate names: conserved hypothetical protein b1344

C: Species: Escherichia coli

C: Date: 10-Sep-1999 #seq: 11 #ref: 1999 #text_change: 10-Sep-1999

C: Accession: C64884

R: Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A: Rose, D.; Mau, B.; Sano, Y.

Science 277, 1453-1462, 1997

Alt: The complete genome sequence of Escherichia coli K-12

A: Reference number: 564711, MIM: 614267

A: Accession: C64884

A: Status: preliminary; protein 1453-1462; for seqm; translation: 1-462

A: Molecule type: DNA

A: Residues: 1-461 (FAT)

A: Cross references: JGI-DOE/Genome Center, MIM: 614267, EMBL: C64884, NCBI: C64884

A: Experimental source: strain: E. coli K-12, strain: H1250

C: Genetics:

A: Gene: y340

C: Superfamily: conserved hypothetical protein

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Query Match

33.1% Score 45; DB 2; Length 669

Best Local Similarity: 50.0% (Prod. No. 25)

Matches: 8; Conservative: 3; Mismatches: 3; Gaps: 0

7 TQKQKPKLVDFLOSL 22

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 25)

Matches: 8; Conservative: 3; Mismatches: 3; Gaps: 0

7 TQKQKPKLVDFLOSL 22

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 25)

Matches: 8; Conservative: 3; Mismatches: 3; Gaps: 0

7 TQKQKPKLVDFLOSL 22

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 25)

Matches: 8; Conservative: 3; Mismatches: 3; Gaps: 0

7 TQKQKPKLVDFLOSL 22

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 25)

Matches: 8; Conservative: 3; Mismatches: 3; Gaps: 0

7 TQKQKPKLVDFLOSL 22

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 25)

Matches: 8; Conservative: 3; Mismatches: 3; Gaps: 0

7 TQKQKPKLVDFLOSL 22

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 25)

Matches: 8; Conservative: 3; Mismatches: 3; Gaps: 0

7 TQKQKPKLVDFLOSL 22

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 25)

Matches: 8; Conservative: 3; Mismatches: 3; Gaps: 0

7 TQKQKPKLVDFLOSL 22

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 25)

Matches: 8; Conservative: 3; Mismatches: 3; Gaps: 0

RESULT 8

138026

Matrix metalloproteinase-13 (MMP-13) (MMP-13)

N: Alternate names: conserved hypothetical protein b1344

C: Species: Homo sapiens (man)

C: Date: 10-Sep-1999 #seq: 11 #ref: 1999 #text_change: 10-Sep-1999

C: Accession: C64884

R: Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A: Rose, D.; Mau, B.; Sano, Y.

Science 277, 1453-1462, 1997

Alt: The complete genome sequence of Escherichia coli K-12

A: Reference number: 564711, MIM: 614267

A: Accession: C64884

A: Status: preliminary; protein 1453-1462; for seqm; translation: 1-462

A: Molecule type: DNA

A: Residues: 1-461 (FAT)

A: Cross references: JGI-DOE/Genome Center, MIM: 614267, EMBL: C64884, NCBI: C64884

A: Experimental source: strain: E. coli K-12, strain: H1250

C: Genetics:

A: Gene: y340

C: Superfamily: conserved hypothetical protein

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

RESULT 9

138026

Matrix metalloproteinase-13 (MMP-13) (MMP-13)

N: Alternate names: conserved hypothetical protein b1344

C: Species: Homo sapiens (man)

C: Date: 10-Sep-1999 #seq: 11 #ref: 1999 #text_change: 10-Sep-1999

C: Accession: C64884

R: Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A: Rose, D.; Mau, B.; Sano, Y.

Science 277, 1453-1462, 1997

Alt: The complete genome sequence of Escherichia coli K-12

A: Reference number: 564711, MIM: 614267

A: Accession: C64884

A: Status: preliminary; protein 1453-1462; for seqm; translation: 1-462

A: Molecule type: DNA

A: Residues: 1-461 (FAT)

A: Cross references: JGI-DOE/Genome Center, MIM: 614267, EMBL: C64884, NCBI: C64884

A: Experimental source: strain: E. coli K-12, strain: H1250

C: Genetics:

A: Gene: y340

C: Superfamily: conserved hypothetical protein

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

RESULT 10

138026

Matrix metalloproteinase-13 (MMP-13) (MMP-13)

N: Alternate names: conserved hypothetical protein b1344

C: Species: Homo sapiens (man)

C: Date: 10-Sep-1999 #seq: 11 #ref: 1999 #text_change: 10-Sep-1999

C: Accession: C64884

R: Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A: Rose, D.; Mau, B.; Sano, Y.

Science 277, 1453-1462, 1997

Alt: The complete genome sequence of Escherichia coli K-12

A: Reference number: 564711, MIM: 614267

A: Accession: C64884

A: Status: preliminary; protein 1453-1462; for seqm; translation: 1-462

A: Molecule type: DNA

A: Residues: 1-461 (FAT)

A: Cross references: JGI-DOE/Genome Center, MIM: 614267, EMBL: C64884, NCBI: C64884

A: Experimental source: strain: E. coli K-12, strain: H1250

C: Genetics:

A: Gene: y340

C: Superfamily: conserved hypothetical protein

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12 GPRKLVDFLOSL 25

DB

Query Match

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Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

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Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

12 GPRKLVDFLOSL 25

DB

Query Match

Best Local Similarity: 50.0% (Prod. No. 917)

Matches: 7; Conservative: 2; Mismatches: 2; Gaps: 0

